

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Ile Gly His Asp Cys Ala His
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Val Gly His Asp Cys Gly His
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His Asn Ala His His
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (peptide)

466T60-466T60

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

His Asn Tyr Leu His His
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Arg Thr His His
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Arg Arg His His
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Asp Arg His His
1 5

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Gln Ile Glu His His
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Gln Val Thr His His
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

His Val Ile His His
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

His Val Ala His His
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Ile Pro His His
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

His Val Pro His His
1 5

466T662) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 48..1406

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 48..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCCAAAAAT TTTCATTGTT CTCCATCTGG ACCACAGCAT CCACACA	ATG GAG GGC	56
	Met Glu Gly	
	1	
GAA GCT AAG AAG TAT ATC ACG GCG GAG GAC CTC CGC CGC CAC AAC AAG		104
Glu Ala Lys Lys Tyr Ile Thr Ala Glu Asp Leu Arg Arg His Asn Lys		
5 10 15		
TCC GGC GAT CTC TGG ATC TCC ATC CAG GGC AAG GTC TAC GAC TGC TCT		152

Ser 20	Gly	Asp	Leu	Trp	Ile 25	Ser	Ile	Gln	Gly	Lys 30	Val	Tyr	Asp	Cys	Ser 35	
CGG	TGG	GCG	GCG	GAG	CAC	CCC	GGC	GGC	GAG	GTC	CCG	CTC	CTC	AGT	CTG	200
Arg	Trp	Ala	Ala	Glu 40	His	Pro	Gly	Gly	Glu 45	Val	Pro	Leu	Leu	Ser 50	Leu	
GCC	GGC	CAG	GAC	GTC	ACC	GAC	GCC	TTC	ATT	GCG	TAC	CAC	CCG	GGC	ACG	248
Ala	Gly	Gln	Asp 55	Val	Thr	Asp	Ala	Phe 60	Ile	Ala	Tyr	His	Pro 65	Gly	Thr	
GCG	TGG	CGG	CAT	CTG	GAT	CCG	CTC	TTC	ACC	GGC	TAC	TAC	TAC	CTC	AAG	296
Ala	Trp	Arg 70	His	Leu	Asp	Pro	Leu 75	Phe	Thr	Gly	Tyr	Tyr 80	Tyr	Leu	Lys	
GAC	TTC	GAA	GTG	TCG	GAG	ATC	TCC	AAG	GAC	TAC	CGG	AGG	CTT	TTG	AAC	344
Asp 85	Phe	Glu	Val	Ser	Glu 90	Ile	Ser	Lys	Asp	Tyr	Arg 95	Arg	Leu	Leu	Asn	
GAG	ATG	TCG	CGG	TCC	GGG	ATC	TTC	GAG	AAG	AAG	GGC	CAC	CAC	ATC	ATG	392
Glu 100	Met	Ser	Arg	Ser	Gly 105	Ile	Phe	Glu	Lys	Lys 110	Gly	His	His	Ile	Met 115	
TGG	ACG	TTC	GTC	GGC	GTT	GCG	GTC	ATG	ATG	GCG	GCA	ATC	GTC	TAC	GGC	440
Trp	Thr	Phe	Val 120	Gly	Val	Ala	Val	Met	Met 125	Ala	Ala	Ile	Val	Tyr 130	Gly	
GTG	CTG	GCG	TCG	GAG	TCC	GTC	GGA	GTT	CAC	ATG	CTC	TGC	GGC	GCA	CTG	488
Val	Leu	Ala	Ser 135	Glu	Ser	Val	Gly	Val 140	His	Met	Leu	Cys	Gly 145	Ala	Leu	
CTG	GGC	TTG	CTG	TGG	ATC	CAA	GCC	GCG	TAT	GTG	GGC	CAT	GAC	TCC	GGC	536
Leu	Gly	Leu 150	Leu	Trp	Ile	Gln	Ala 155	Ala	Tyr	Val	Gly	His 160	Asp	Ser	Gly	
CAT	TAC	CAG	GTG	ATG	CCA	ACC	CGT	GGA	TAC	AAC	AGA	ATC	ACG	CAA	CTC	584
His	Tyr 165	Gln	Val	Met	Pro	Thr 170	Arg	Gly	Tyr	Asn 175	Arg	Ile	Thr	Gln	Leu	
ATA	GCA	GGC	AAC	ATC	CTA	ACC	GGA	ATC	AGC	ATC	GCG	TGG	TGG	AAG	TGG	632
Ile 180	Ala	Gly	Asn	Ile	Leu 185	Thr	Gly	Ile	Ser	Ile 190	Ala	Trp	Trp	Lys	Trp 195	
ACC	CAC	AAC	GCC	CAC	CAC	CTC	GCC	TGC	AAC	AGC	CTC	GAC	TAC	GAC	CCC	680
Thr	His	Asn	Ala 200	His	His	Leu	Ala	Cys	Asn 205	Ser	Leu	Asp	Tyr	Asp 210	Pro	
GAC	CTC	CAG	CAC	ATC	CCC	GTA	TTC	GCC	GTC	TCC	ACC	CGA	CTC	TTC	AAC	728
Asp	Leu	Gln	His 215	Ile	Pro	Val	Phe	Ala 220	Val	Ser	Thr	Arg	Leu 225	Phe	Asn	
TCC	ATC	ACC	TCG	GTC	TTC	TAT	GGC	CGA	GTC	CTG	AAA	TTC	GAC	GAA	GTG	776
Ser	Ile	Thr 230	Ser	Val	Phe	Tyr	Gly 235	Arg	Val	Leu	Lys	Phe 240	Asp	Glu	Val	

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GCA	CGG	TTC	CTA	GTC	AGC	TAC	CAG	CAC	TGG	ACC	TAC	TAC	CCG	GTC	ATG	824
Ala	Arg	Phe	Leu	Val	Ser	Tyr	Gln	His	Trp	Thr	Tyr	Tyr	Pro	Val	Met	
	245					250					255					
ATC	TTC	GGC	CGA	GTC	AAC	CTC	TTC	ATC	CAG	ACC	TTT	TTA	TTG	CTC	CTC	872
Ile	Phe	Gly	Arg	Val	Asn	Leu	Phe	Ile	Gln	Thr	Phe	Leu	Leu	Leu	Leu	
260					265					270					275	
ACC	AGG	CGC	GAC	GTC	CCT	GAC	CGC	GCT	CTA	AAC	TTA	ATG	GGT	ATC	GCG	920
Thr	Arg	Arg	Asp	Val	Pro	Asp	Arg	Ala	Leu	Asn	Leu	Met	Gly	Ile	Ala	
				280					285					290		
GTT	TTC	TGG	ACG	TGG	TTC	CCG	CTC	TTC	GTA	TCT	TGT	CTC	CCG	AAC	TGG	968
Val	Phe	Trp	Thr	Trp	Phe	Pro	Leu	Phe	Val	Ser	Cys	Leu	Pro	Asn	Trp	
			295					300					305			
CCT	GAA	CGG	TTC	GGG	TTC	GTC	CTC	ATC	AGC	TTT	GCG	GTC	ACG	GCG	ATC	1016
Pro	Glu	Arg	Phe	Gly	Phe	Val	Leu	Ile	Ser	Phe	Ala	Val	Thr	Ala	Ile	
		310					315					320				
CAG	CAC	GTC	CAG	TTC	ACG	CTC	AAC	CAC	TTC	TCC	GGC	GAC	ACA	TAC	GTG	1064
Gln	His	Val	Gln	Phe	Thr	Leu	Asn	His	Phe	Ser	Gly	Asp	Thr	Tyr	Val	
	325					330					335					
GGC	CCC	CCC	AAG	GGC	GAC	AAC	TGG	TTC	GAG	AAG	CAG	ACG	AAA	GGG	ACG	1112
Gly	Pro	Pro	Lys	Gly	Asp	Asn	Trp	Phe	Glu	Lys	Gln	Thr	Lys	Gly	Thr	
340					345					350					355	
ATC	GAT	ATC	ACG	TGC	CCA	CCG	TGG	ATG	GAC	TGG	TTC	TTT	GGT	GGG	CTG	1160
Ile	Asp	Ile	Thr	Cys	Pro	Pro	Trp	Met	Asp	Trp	Phe	Phe	Gly	Gly	Leu	
				360					365					370		
CAG	TTC	CAG	TTG	GAG	CAC	CAC	TTG	TTC	CCT	AGG	CTG	CCG	CGT	GGG	CAG	1208
Gln	Phe	Gln	Leu	Glu	His	His	Leu	Phe	Pro	Arg	Leu	Pro	Arg	Gly	Gln	
			375					380					385			
CTT	AGG	AAG	ATT	GCG	CCC	TTG	GCT	CGG	GAC	TTG	TGT	AAG	AAG	CAC	GGG	1256
Leu	Arg	Lys	Ile	Ala	Pro	Leu	Ala	Arg	Asp	Leu	Cys	Lys	Lys	His	Gly	
		390					395					400				
ATG	CCG	TAT	AGG	AGC	TTC	GGG	TTT	TGG	GAC	GAC	GCT	AAT	GTC	AGG	ACA	1304
Met	Pro	Tyr	Arg	Ser	Phe	Gly	Phe	Trp	Asp	Asp	Ala	Asn	Val	Arg	Thr	
	405					410					415					
ATT	CGG	ACG	CTG	AGG	GAT	GCG	GCG	GTT	CAG	GCG	CGT	GAC	CTT	AAT	TCG	1352
Ile	Arg	Thr	Leu	Arg	Asp	Ala	Ala	Val	Gln	Ala	Arg	Asp	Leu	Asn	Ser	
420					425					430					435	
GCC	CCG	TGC	CCT	AAG	AAA	CTT	GGG	TAT	GGG	GAA	GCT	TAT	AAC	ACC	CAT	1400
Ala	Pro	Cys	Pro	Lys	Lys	Leu	Gly	Tyr	Gly	Glu	Ala	Tyr	Asn	Thr	His	
				440					445					450		
GGT	TGA	TTGTGGTTTT	GTGTTGTGGG	TTGGAGGATC	TTCTTATTAT	TGATTTATGT										1456
Gly	*															

CCACAATATT GAACTGAATA ACCATGGAAG GCACTACGTT CAGCTTAACT TTGCTTAACT 1516
 TTGCTAGCTG GTTGC GTTCC CTTGTTGGGG GCAAAGTGCA GTATTTATTT TCTTATCCCA 1576
 TGTACTTTTT GATTATTGTT CTTATTCGTA TCATAAATAA TTTATTATTG ATTAATTTTT 1636
 GTTGTAGTTG GGTGTCTATA GCAAGTTTAT AATACTGAGA TATATTTTTT TGGTAAAAAA 1696
 AAAAAA 1702

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Gly Glu Ala Lys Lys Tyr Ile Thr Ala Glu Asp Leu Arg Arg
 1 5 10 15
 His Asn Lys Ser Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Val Tyr
 20 25 30
 Asp Cys Ser Arg Trp Ala Ala Glu His Pro Gly Gly Glu Val Pro Leu
 35 40 45
 Leu Ser Leu Ala Gly Gln Asp Val Thr Asp Ala Phe Ile Ala Tyr His
 50 55 60
 Pro Gly Thr Ala Trp Arg His Leu Asp Pro Leu Phe Thr Gly Tyr Tyr
 65 70 75 80
 Tyr Leu Lys Asp Phe Glu Val Ser Glu Ile Ser Lys Asp Tyr Arg Arg
 85 90 95
 Leu Leu Asn Glu Met Ser Arg Ser Gly Ile Phe Glu Lys Lys Gly His
 100 105 110
 His Ile Met Trp Thr Phe Val Gly Val Ala Val Met Met Ala Ala Ile
 115 120 125
 Val Tyr Gly Val Leu Ala Ser Glu Ser Val Gly Val His Met Leu Cys
 130 135 140
 Gly Ala Leu Leu Gly Leu Leu Trp Ile Gln Ala Ala Tyr Val Gly His
 145 150 155 160
 Asp Ser Gly His Tyr Gln Val Met Pro Thr Arg Gly Tyr Asn Arg Ile
 165 170 175

Thr Gln Leu Ile Ala Gly Asn Ile Leu Thr Gly Ile Ser Ile Ala Trp
180 185 190

Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp
195 200 205

Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser Thr Arg
210 215 220

Leu Phe Asn Ser Ile Thr Ser Val Phe Tyr Gly Arg Val Leu Lys Phe
225 230 235 240

Asp Glu Val Ala Arg Phe Leu Val Ser Tyr Gln His Trp Thr Tyr Tyr
245 250 255

Pro Val Met Ile Phe Gly Arg Val Asn Leu Phe Ile Gln Thr Phe Leu
260 265 270

Leu Leu Leu Thr Arg Arg Asp Val Pro Asp Arg Ala Leu Asn Leu Met
275 280 285

Gly Ile Ala Val Phe Trp Thr Trp Phe Pro Leu Phe Val Ser Cys Leu
290 295 300

Pro Asn Trp Pro Glu Arg Phe Gly Phe Val Leu Ile Ser Phe Ala Val
305 310 315 320

Thr Ala Ile Gln His Val Gln Phe Thr Leu Asn His Phe Ser Gly Asp
325 330 335

Thr Tyr Val Gly Pro Pro Lys Gly Asp Asn Trp Phe Glu Lys Gln Thr
340 345 350

Lys Gly Thr Ile Asp Ile Thr Cys Pro Pro Trp Met Asp Trp Phe Phe
355 360 365

Gly Gly Leu Gln Phe Gln Leu Glu His His Leu Phe Pro Arg Leu Pro
370 375 380

Arg Gly Gln Leu Arg Lys Ile Ala Pro Leu Ala Arg Asp Leu Cys Lys
385 390 395 400

Lys His Gly Met Pro Tyr Arg Ser Phe Gly Phe Trp Asp Asp Ala Asn
405 410 415

Val Arg Thr Ile Arg Thr Leu Arg Asp Ala Ala Val Gln Ala Arg Asp
420 425 430

Leu Asn Ser Ala Pro Cys Pro Lys Lys Leu Gly Tyr Gly Glu Ala Tyr
435 440 445

Asn Thr His Gly *
450